

0300

#3



O I P E

## RAW SEQUENCE LISTING

DATE: 02/27/2002

PATENT APPLICATION: US/10/071,275

TIME: 13:48:34

Input Set : A:\10448-139001.txt

Output Set: N:\CRF3\02272002\J071275.raw

ENTERED

4 <110> APPLICANT: Meyers, Rachel E.  
 6 <120> TITLE OF INVENTION: 80091, A NOVEL HUMAN UBIQUITIN  
 7 CARBOXY-TERMINAL HYDROLASE FAMILY MEMBER AND USES THEREOF  
 10 <130> FILE REFERENCE: 10448-139001  
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/071,275  
 C--> 12 <141> CURRENT FILING DATE: 2002-02-07  
 12 <150> PRIOR APPLICATION NUMBER: 60/267,054  
 13 <151> PRIOR FILING DATE: 2001-02-07  
 15 <160> NUMBER OF SEQ ID NOS: 7  
 17 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 19 <210> SEQ ID NO: 1  
 20 <211> LENGTH: 3954  
 21 <212> TYPE: DNA  
 22 <213> ORGANISM: Homo sapiens  
 24 <220> FEATURE:  
 25 <221> NAME/KEY: CDS  
 26 <222> LOCATION: (1)...(3951)  
 28 <400> SEQUENCE: 1  
 29 atg gtg gct gat gcc tgt aat ccc aac agt ttg gga gac tgg gga gga 48  
 30 Met Val Ala Asp Ala Cys Asn Pro Asn Ser Leu Gly Asp Trp Gly Gly  
 31 1 5 10 15  
 33 aga tca ttt gag gcc agg agt ttg aga cca gcc tgg gct caa gca gtc 96  
 34 Arg Ser Phe Glu Ala Arg Ser Leu Arg Pro Ala Trp Ala Gln Ala Val  
 35 20 25 30  
 37 ctg cct cag cct ccc aaa gtg ctg gga tta cag atg ggt cat ctt act 144  
 38 Leu Pro Gln Pro Pro Lys Val Leu Gly Leu Gln Met Gly His Leu Thr  
 39 35 40 45  
 41 ctg gaa gac tat cag atc tgg agt gtg aaa aat gtt ctt gcc aat gag 192  
 42 Leu Glu Asp Tyr Gln Ile Trp Ser Val Lys Asn Val Leu Ala Asn Glu  
 43 50 55 60  
 45 ttt ttg aac ctc ctt ttc cag gtg tgt cac ata gtt ctg ggg tta aga 240  
 46 Phe Leu Asn Leu Leu Phe Gln Val Cys His Ile Val Leu Gly Leu Arg  
 47 65 70 75 80  
 49 cca gct act ccg gaa gaa gaa gga caa att att aga gga tgg tta gaa 288  
 50 Pro Ala Thr Pro Glu Glu Glu Gly Gln Ile Ile Arg Gly Trp Leu Glu  
 51 85 90 95  
 53 cga gag agc agg tat ggt ctg caa gca gga cac aac tgg ttt atc atc 336  
 54 Arg Glu Ser Arg Tyr Gly Leu Gln Ala Gly His Asn Trp Phe Ile Ile  
 55 100 105 110  
 57 tcc atg cag tgg tgg caa cag tgg aaa gaa tat gtc aaa tac gat gcc 384  
 58 Ser Met Gln Trp Trp Gln Gln Trp Lys Glu Tyr Val Lys Tyr Asp Ala  
 59 115 120 125  
 61 aac cct gtg gta att gag cca tca tct gtt ttg aat gga gga aaa tac 432

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62 Asn Pro Val Val Ile Glu Pro Ser Ser Val Leu Asn Gly Gly Lys Tyr
63      130      135      140
65 tca ttt gga act gca gcc cat cct atg gag cag gtc gaa gat aga att      480
66 Ser Phe Gly Thr Ala Ala His Pro Met Glu Gln Val Glu Asp Arg Ile
67 145      150      155      160
69 gga agc agc ctc agt tac gtg aat act aca gaa gag aaa ttt tca gac      528
70 Gly Ser Ser Leu Ser Tyr Val Asn Thr Thr Glu Glu Lys Phe Ser Asp
71      165      170      175
73 aac att tct act gca tct gaa gcc tca gaa act gct ggc agc ggc ttt      576
74 Asn Ile Ser Thr Ala Ser Glu Ala Ser Glu Thr Ala Gly Ser Gly Phe
75      180      185      190
77 ctg tat tct gcc aca cca ggg gca gat gtt tgc ttt gct cga caa cat      624
78 Leu Tyr Ser Ala Thr Pro Gly Ala Asp Val Cys Phe Ala Arg Gln His
79      195      200      205
81 aac act tct gac aat aac aac cag tgt ttg ctg gga gcc aat ggg aat      672
82 Asn Thr Ser Asp Asn Asn Asn Gln Cys Leu Leu Gly Ala Asn Gly Asn
83      210      215      220
85 att ttg ttg cac ctt aac cct cag aaa cca ggg gct att gat aat cag      720
86 Ile Leu Leu His Leu Asn Pro Gln Lys Pro Gly Ala Ile Asp Asn Gln
87 225      230      235      240
89 cca tta gta act caa gaa cca gta aag gct aca tca tta aca cta gaa      768
90 Pro Leu Val Thr Gln Glu Pro Val Lys Ala Thr Ser Leu Thr Leu Glu
91      245      250      255
93 gga gga cga tta aaa cga act cca cag ctg att cat gga aga gac tat      816
94 Gly Gly Arg Leu Lys Arg Thr Pro Gln Leu Ile His Gly Arg Asp Tyr
95      260      265      270
97 gaa atg gtc cca gaa cct gtg tgg aga gca ctt tat cac tgg tat gga      864
98 Glu Met Val Pro Glu Pro Val Trp Arg Ala Leu Tyr His Trp Tyr Gly
99      275      280      285
101 gca aac ctg gcc tta cct aga cca gtt atc aag aac agc aag aca gac      912
102 Ala Asn Leu Ala Leu Pro Arg Pro Val Ile Lys Asn Ser Lys Thr Asp
103      290      295      300
105 atc cca gag ctg gaa tta ttt ccc cgc tat ctt ctc ttc ctg aga cag      960
106 Ile Pro Glu Leu Glu Leu Phe Pro Arg Tyr Leu Leu Phe Leu Arg Gln
107 305      310      315      320
109 cag cct gcc act cgg aca cag cag tct aac atc tgg gtg aat atg gga      1008
110 Gln Pro Ala Thr Arg Thr Gln Gln Ser Asn Ile Trp Val Asn Met Gly
111      325      330      335
113 aat gta cct tct ccg aat gca cct tta aag cgg gta tta gcc tat aca      1056
114 Asn Val Pro Ser Pro Asn Ala Pro Leu Lys Arg Val Leu Ala Tyr Thr
115      340      345      350
117 ggc tgt ttt agt cga atg cag acc atc aag gaa att cac gaa tat cta      1104
118 Gly Cys Phe Ser Arg Met Gln Thr Ile Lys Glu Ile His Glu Tyr Leu
119      355      360      365
121 tct caa aga ctg cgc att aaa gag gaa gat atg cgc ctg tgg cta tac      1152
122 Ser Gln Arg Leu Arg Ile Lys Glu Glu Asp Met Arg Leu Trp Leu Tyr
123      370      375      380
125 aac agt gag aac tac ctt act ctt ctg gat gat gag gat cat aaa ttg      1200
126 Asn Ser Glu Asn Tyr Leu Thr Leu Leu Asp Asp Glu Asp His Lys Leu

```

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127	385		390		395		400	
129	gaa	tat	ttg	aaa	atc	cag	gat	gaa
130	Glu	Tyr	Leu	Lys	Ile	Gln	Asp	Glu
131				405				410
133	aac	aaa	gat	atg	agt	tgg	cct	gag
134	Asn	Lys	Asp	Met	Ser	Trp	Pro	Glu
135				420				425
137	agt	aaa	ata	gat	aga	cac	aag	gtt
138	Ser	Lys	Ile	Asp	Arg	His	Lys	Val
139				435				440
141	cta	agc	aat	ctg	gga	aac	aca	tgc
142	Leu	Ser	Asn	Leu	Gly	Asn	Thr	Cys
143				450				455
145	gtt	agt	aac	aca	cag	cca	ctg	aca
146	Val	Ser	Asn	Thr	Gln	Pro	Leu	Thr
147	465							470
149	ctt	tat	gaa	ctc	aac	agg	aca	aat
150	Leu	Tyr	Glu	Leu	Asn	Arg	Thr	Asn
151								485
153	gct	aaa	tgc	tat	ggg	gat	tta	gtg
154	Ala	Lys	Cys	Tyr	Gly	Asp	Leu	Val
155				500				505
157	aag	aat	gtt	gcc	cca	tta	aag	ctt
158	Lys	Asn	Val	Ala	Pro	Leu	Lys	Leu
159				515				520
161	ccc	agg	ttt	aat	ggg	ttt	cag	caa
162	Pro	Arg	Phe	Asn	Gly	Phe	Gln	Gln
163				530				535
165	ttt	ctc	ttg	gat	ggg	ctt	cat	gaa
166	Phe	Leu	Leu	Asp	Gly	Leu	His	Glu
167	545							550
169	cca	tat	gtg	gaa	ctg	aag	gac	agt
170	Pro	Tyr	Val	Glu	Leu	Lys	Asp	Ser
171								565
173	gct	gca	gag	gcc	tgg	gac	aac	cat
174	Ala	Ala	Glu	Ala	Trp	Asp	Asn	His
175				580				585
177	gtg	gat	ttg	ttc	cat	ggg	cag	cta
178	Val	Asp	Leu	Phe	His	Gly	Gln	Leu
179				595				600
181	tgt	ggg	cat	ata	agt	gtc	cga	ttt
182	Cys	Gly	His	Ile	Ser	Val	Arg	Phe
183				610				615
185	cca	cta	cca	atg	gac	agt	tat	atg
186	Pro	Leu	Pro	Met	Asp	Ser	Tyr	Met
187	625							630
189	tta	gat	ggg	act	acc	cct	gta	cgg
190	Leu	Asp	Gly	Thr	Thr	Pro	Val	Arg
191				645				650

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193	gaa	aag	tac	aca	ggt	tta	aaa	aaa	cag	ctg	agt	gat	ctc	tgt	gga	ctt	2016
194	Glu	Lys	Tyr	Thr	Gly	Leu	Lys	Lys	Gln	Leu	Ser	Asp	Leu	Cys	Gly	Leu	
195				660					665				670				
197	aat	tca	gaa	caa	atc	ctt	cta	gca	gaa	gta	cat	ggt	tcc	aac	ata	aag	2064
198	Asn	Ser	Glu	Gln	Ile	Leu	Leu	Ala	Glu	Val	His	Gly	Ser	Asn	Ile	Lys	
199			675					680					685				
201	aac	ttt	cct	cag	gac	aac	caa	aaa	gta	cga	ctc	tca	gtg	agt	gga	ttt	2112
202	Asn	Phe	Pro	Gln	Asp	Asn	Gln	Lys	Val	Arg	Leu	Ser	Val	Ser	Gly	Phe	
203			690					695					700				
205	ttg	tgt	gca	ttt	gaa	att	cct	gtc	cct	gtg	tct	cca	att	tca	gct	tct	2160
206	Leu	Cys	Ala	Phe	Glu	Ile	Pro	Val	Pro	Val	Ser	Pro	Ile	Ser	Ala	Ser	
207	705					710					715				720		
209	agt	cca	aca	cag	aca	gat	ttc	tcc	tct	tcg	cca	tct	aca	aat	gaa	atg	2208
210	Ser	Pro	Thr	Gln	Thr	Asp	Phe	Ser	Ser	Ser	Pro	Ser	Thr	Asn	Glu	Met	
211						725					730				735		
213	ttc	acc	cta	act	acc	aat	ggg	gac	cta	ccc	cga	cca	ata	ttc	atc	ccc	2256
214	Phe	Thr	Leu	Thr	Thr	Asn	Gly	Asp	Leu	Pro	Arg	Pro	Ile	Phe	Ile	Pro	
215				740					745					750			
217	aat	gga	atg	cca	aac	act	gtt	gtg	cca	tgt	gga	act	gag	aag	aac	ttc	2304
218	Asn	Gly	Met	Pro	Asn	Thr	Val	Val	Pro	Cys	Gly	Thr	Glu	Lys	Asn	Phe	
219			755					760					765				
221	aca	aat	gga	atg	gtt	aat	ggg	cac	atg	cca	tct	ctt	cct	gac	agc	ccc	2352
222	Thr	Asn	Gly	Met	Val	Asn	Gly	His	Met	Pro	Ser	Leu	Pro	Asp	Ser	Pro	
223		770					775					780					
225	ttt	aca	ggt	tac	atc	att	gca	gtc	cac	cga	aaa	atg	atg	agg	aca	gaa	2400
226	Phe	Thr	Gly	Tyr	Ile	Ile	Ala	Val	His	Arg	Lys	Met	Met	Arg	Thr	Glu	
227	785					790					795				800		
229	ctg	tat	ttc	ctg	tca	tct	cag	aag	aat	cgc	ccc	agc	ctc	ttt	gga	atg	2448
230	Leu	Tyr	Phe	Leu	Ser	Ser	Gln	Lys	Asn	Arg	Pro	Ser	Leu	Phe	Gly	Met	
231						805				810					815		
233	cca	ttg	att	gtt	cca	tgt	act	gtg	cat	acc	cgg	aag	aaa	gac	cta	tat	2496
234	Pro	Leu	Ile	Val	Pro	Cys	Thr	Val	His	Thr	Arg	Lys	Lys	Asp	Leu	Tyr	
235				820					825					830			
237	gat	gcg	gtt	tggt	att	caa	gta	tcc	cgg	tta	gcg	agc	cca	ctc	cca	cct	2544
238	Asp	Ala	Val	Trp	Ile	Gln	Val	Ser	Arg	Leu	Ala	Ser	Pro	Leu	Pro	Pro	
239			835					840					845				
241	cag	gaa	gct	agt	aat	cat	gcc	cag	gat	tgt	gac	gac	agt	atg	ggc	tat	2592
242	Gln	Glu	Ala	Ser	Asn	His	Ala	Gln	Asp	Cys	Asp	Asp	Ser	Met	Gly	Tyr	
243		850					855					860					
245	caa	tat	cca	ttc	act	cta	cga	gtt	gtg	cag	aaa	gat	ggg	aac	tcc	tgt	2640
246	Gln	Tyr	Pro	Phe	Thr	Leu	Arg	Val	Val	Gln	Lys	Asp	Gly	Asn	Ser	Cys	
247	865					870					875				880		
249	gct	tggt	tggt	cca	tggt	tat	aga	ttt	tggt	aga	ggc	tgt	aaa	att	gat	tgt	2688
250	Ala	Trp	Cys	Pro	Trp	Tyr	Arg	Phe	Cys	Arg	Gly	Cys	Lys	Ile	Asp	Cys	
251						885					890				895		
253	ggg	gaa	gac	aga	gct	ttc	att	gga	aat	gcc	tat	atc	gct	gtg	gat	tggt	2736
254	Gly	Glu	Asp	Arg	Ala	Phe	Ile	Gly	Asn	Ala	Tyr	Ile	Ala	Val	Asp	Trp	
255			900						905					910			
257	gat	ccc	aca	gcc	ctt	cac	ctt	cgc	tat	caa	aca	tcc	cag	gaa	agg	gtt	2784

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
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Output Set: N:\CRF3\02272002\J071275.raw

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258 Asp Pro Thr Ala Leu His Leu Arg Tyr Gln Thr Ser Gln Glu Arg Val
259          915          920          925
261 gta gat gag cat gag agt gtg gag cag agt cgg cga gcg caa gcc gag      2832
262 Val Asp Glu His Glu Ser Val Glu Gln Ser Arg Arg Ala Gln Ala Glu
263          930          935          940
265 ccc atc aac ctg gac agc tgt ctc cgt gct ttc acc agt gag gaa gag      2880
266 Pro Ile Asn Leu Asp Ser Cys Leu Arg Ala Phe Thr Ser Glu Glu Glu
267 945          950          955          960
269 cta ggg gaa aat gag atg tac tac tgt tcc aag tgt aag acc cac tgc      2928
270 Leu Gly Glu Asn Glu Met Tyr Tyr Cys Ser Lys Cys Lys Thr His Cys
271          965          970          975
273 tta gca aca aag aag ctg gat ctc tgg agg ctt cca ccc atc ctg att      2976
274 Leu Ala Thr Lys Lys Leu Asp Leu Trp Arg Leu Pro Pro Ile Leu Ile
275          980          985          990
277 att cac ctt aag cga ttt caa ttt gta aat ggt cgg tgg ata aaa tca      3024
278 Ile His Leu Lys Arg Phe Gln Phe Val Asn Gly Arg Trp Ile Lys Ser
279          995          1000          1005
281 cag aaa att gtc aaa ttt cct cgg gaa agt ttt gat cca agt gct ttt      3072
282 Gln Lys Ile Val Lys Phe Pro Arg Glu Ser Phe Asp Pro Ser Ala Phe
283          1010          1015          1020
285 ttg gta cca aga gac ccg gct ctc tgc cag cat aaa cca ctc aca ccc      3120
286 Leu Val Pro Arg Asp Pro Ala Leu Cys Gln His Lys Pro Leu Thr Pro
287 1025          1030          1035          1040
289 cag ggg gat gag ctc tct gag ccc agg att ctg gca agg gag gtg aag      3168
290 Gln Gly Asp Glu Leu Ser Glu Pro Arg Ile Leu Ala Arg Glu Val Lys
291          1045          1050          1055
293 aaa gtg gat gcg cag agt tcg gct ggg gaa gag gac gtg ctc ctg agc      3216
294 Lys Val Asp Ala Gln Ser Ser Ala Gly Glu Glu Asp Val Leu Leu Ser
295          1060          1065          1070
297 aaa agc cca tcc tca ctc agc gct aac atc atc agc agc ccg aaa ggt      3264
298 Lys Ser Pro Ser Ser Leu Ser Ala Asn Ile Ile Ser Ser Pro Lys Gly
299          1075          1080          1085
301 tct cct tct tca tca aga aaa agt gga acc agc tgt ccc tcc agc aaa      3312
302 Ser Pro Ser Ser Ser Arg Lys Ser Gly Thr Ser Cys Pro Ser Ser Lys
303          1090          1095          1100
305 aac agc agc cct aat agc agc cca cgg act ttg ggg agg agc aaa ggg      3360
306 Asn Ser Ser Pro Asn Ser Ser Pro Arg Thr Leu Gly Arg Ser Lys Gly
307 1105          1110          1115          1120
309 agg ctc cgg ctg ccc cag att ggc agc aaa aat aaa ctg tca agt agt      3408
310 Arg Leu Arg Leu Pro Gln Ile Gly Ser Lys Asn Lys Leu Ser Ser Ser
311          1125          1130          1135
313 aaa gag aac ttg gat gcc agc aaa gaa aat ggg gct ggg cag ata tgt      3456
314 Lys Glu Asn Leu Asp Ala Ser Lys Glu Asn Gly Ala Gly Gln Ile Cys
315          1140          1145          1150
317 gag ctg gct gac gcc ttg agt cga ggg cat gtg ctg ggg ggc agc caa      3504
318 Glu Leu Ala Asp Ala Leu Ser Arg Gly His Val Leu Gly Gly Ser Gln
319          1155          1160          1165
321 cca gag ttg gtc act cct cag gac cat gag gta gct ttg gcc aat gga      3552
322 Pro Glu Leu Val Thr Pro Gln Asp His Glu Val Ala Leu Ala Asn Gly

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 Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

**VERIFICATION SUMMARY**

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:590 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5